

FIG. 1

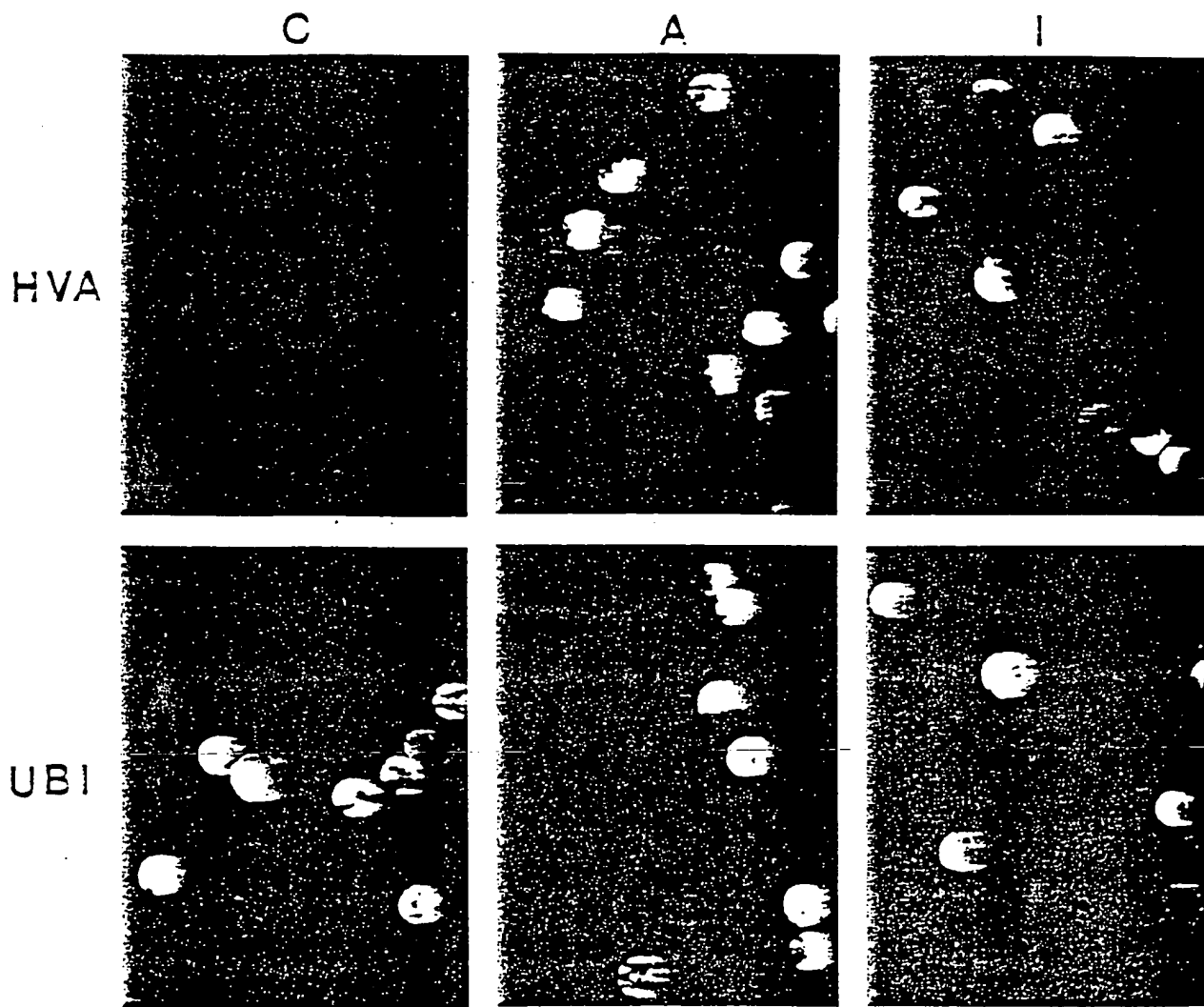


FIG. 2

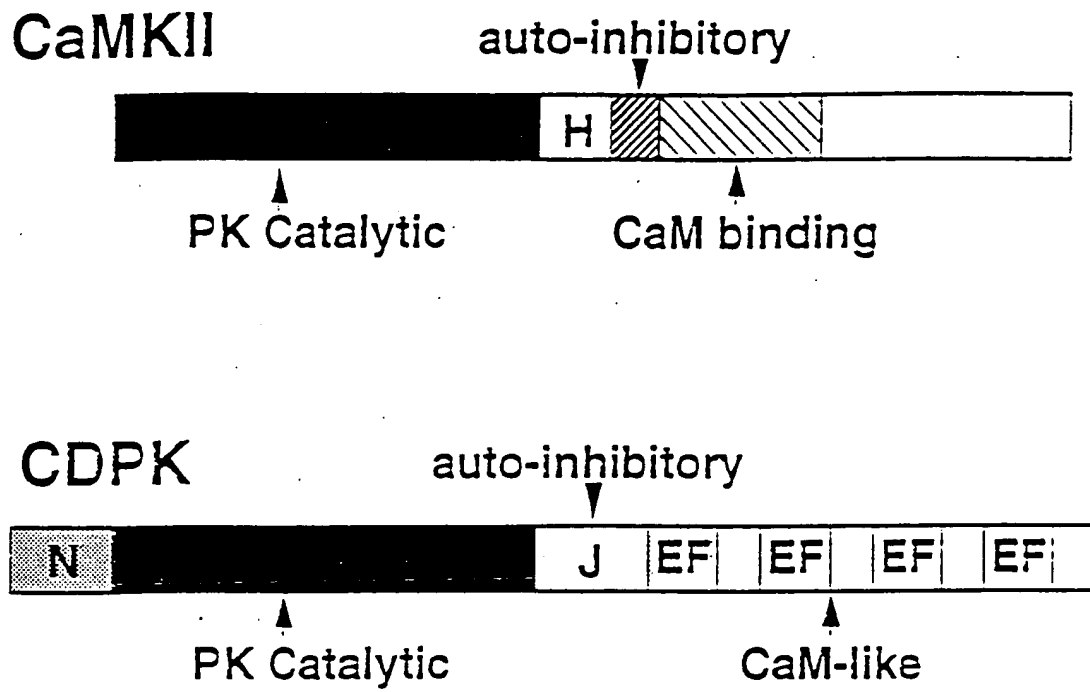


FIG. 3A

Atcdpk	HGHTCVGPR	RGFLQSVSA	MVRPRDGD	ASHNGDIA	EAVSGEIRSR	LSDEVQHKPP	60
Atcdpk1							0
Atcdpk1a							0
Atcdpk2							0
Atcdpk	EQVTTPKPGT	DVETKDRER	TESKPELEE	ISLESKPETK	QETKSETKPE	SKPDPAPKPK	120
Atcdpk1							0
Atcdpk1a							0
Atcdpk2							9
Atcdpk	KPKHHRVSS	AGLRTESVLQ	RKTEHFF	VS	QFGTTF	KTGKEPAC	179
Atcdpk1							40
Atcdpk1a							40
Atcdpk2							55
Atcdpk	SAI	EP	Q	VS	QFGTTF	KTGKEPAC	239
Atcdpk1							100
Atcdpk1a							100
Atcdpk2							115
Atcdpk	IVAR	KA	Q	VS	QFGTTF	KTGKEPAC	299
Atcdpk1							160
Atcdpk1a							160
Atcdpk2							175
Atcdpk	VFYK	QY	Q	VS	QFGTTF	KTGKEPAC	359
Atcdpk1							220
Atcdpk1a							220
Atcdpk2							235
Atcdpk	EQV	Q	Q	VS	QFGTTF	KTGKEPAC	179
Atcdpk1							40
Atcdpk1a							40
Atcdpk2							55

FIG. 3B

PK Constructs

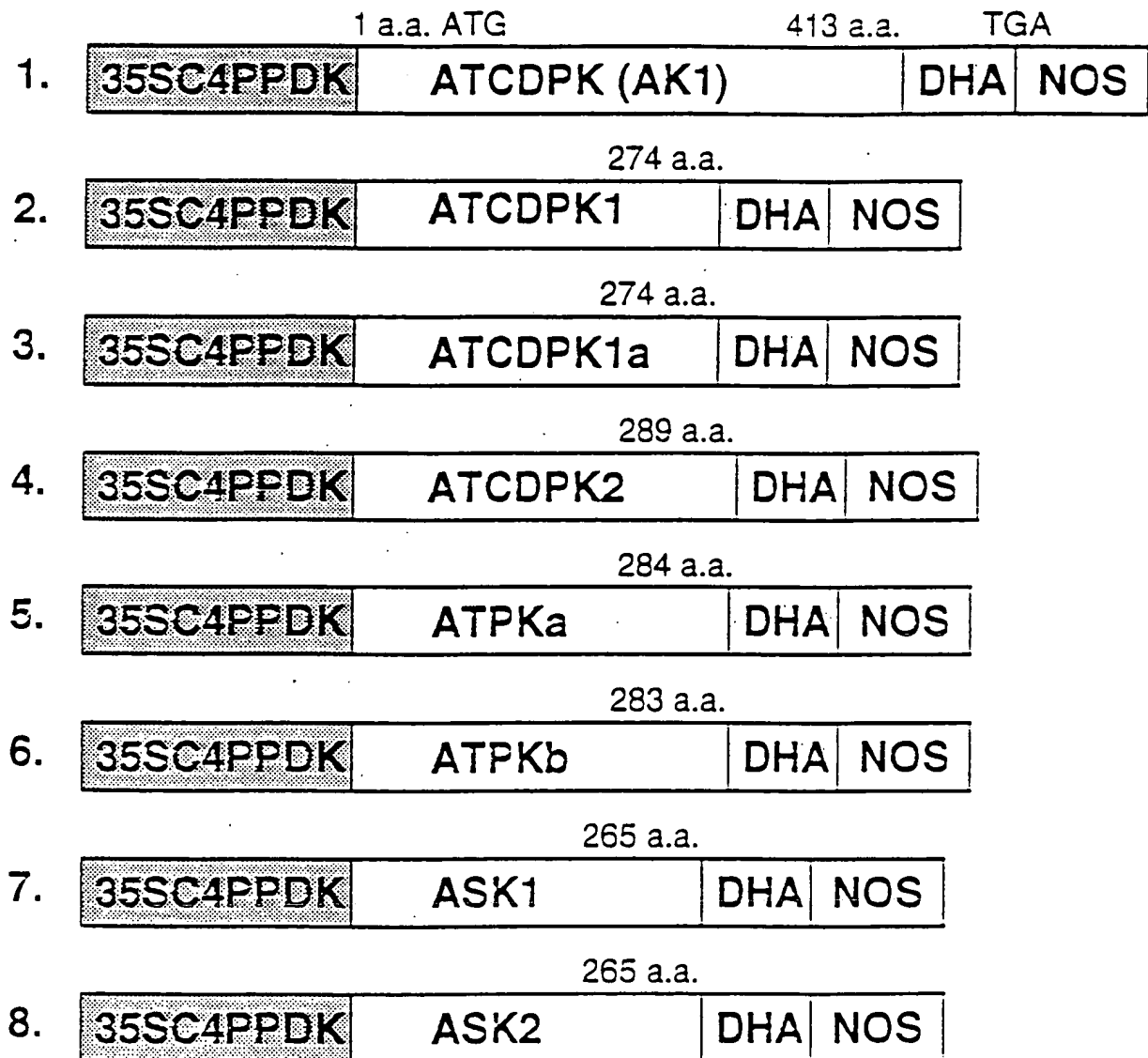


FIG. 3C

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d

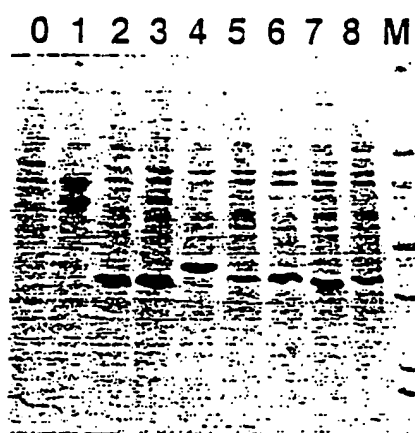


FIG. 3D

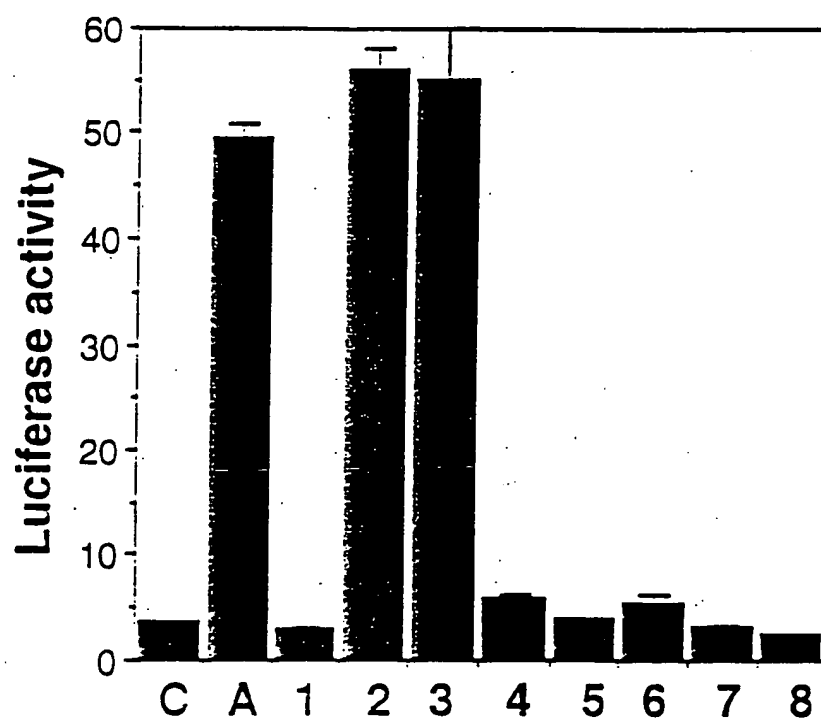


FIG. 3E

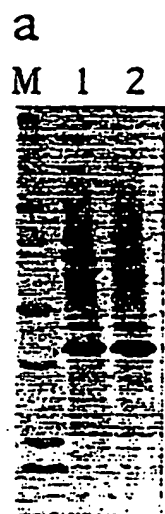
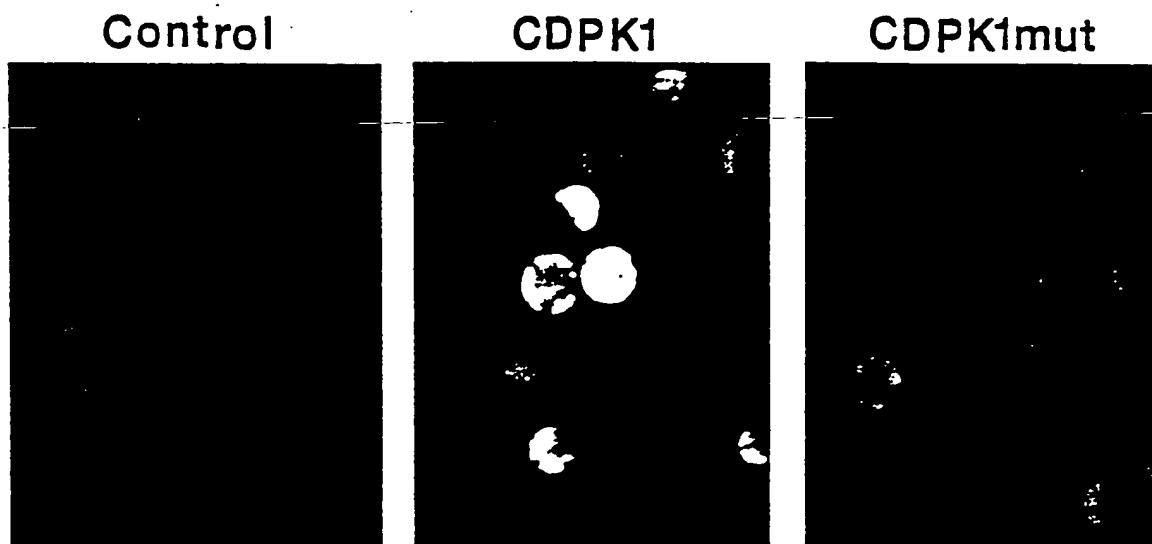


FIG. 4A

FIG. 4B



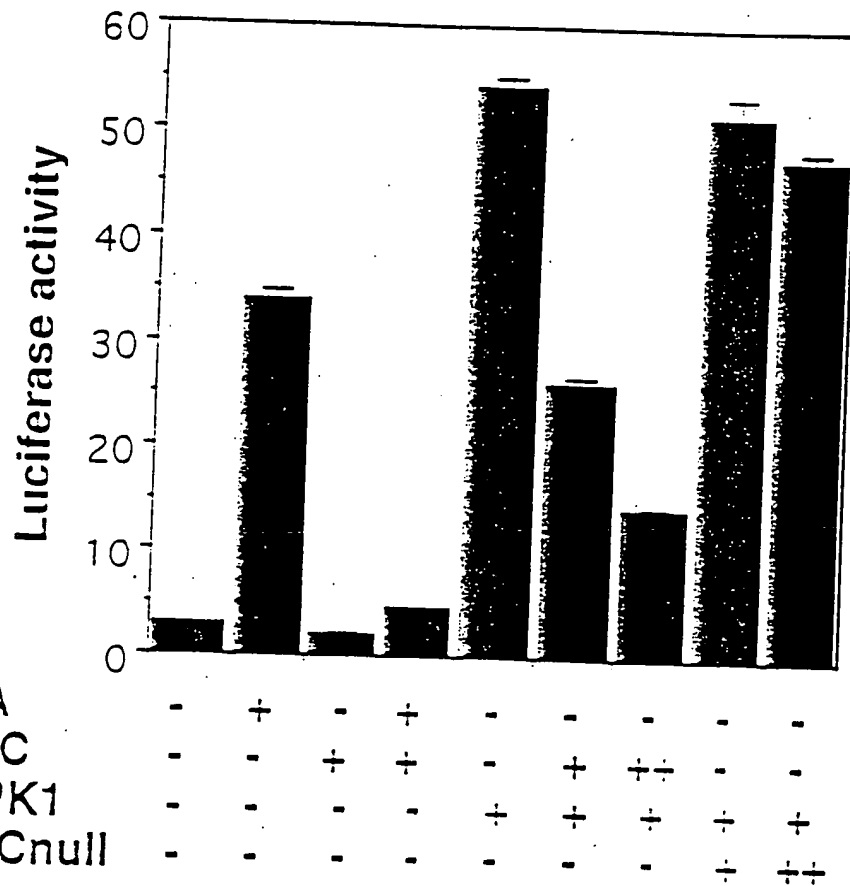


FIG. 4C

A model of stress signalling in plant cells

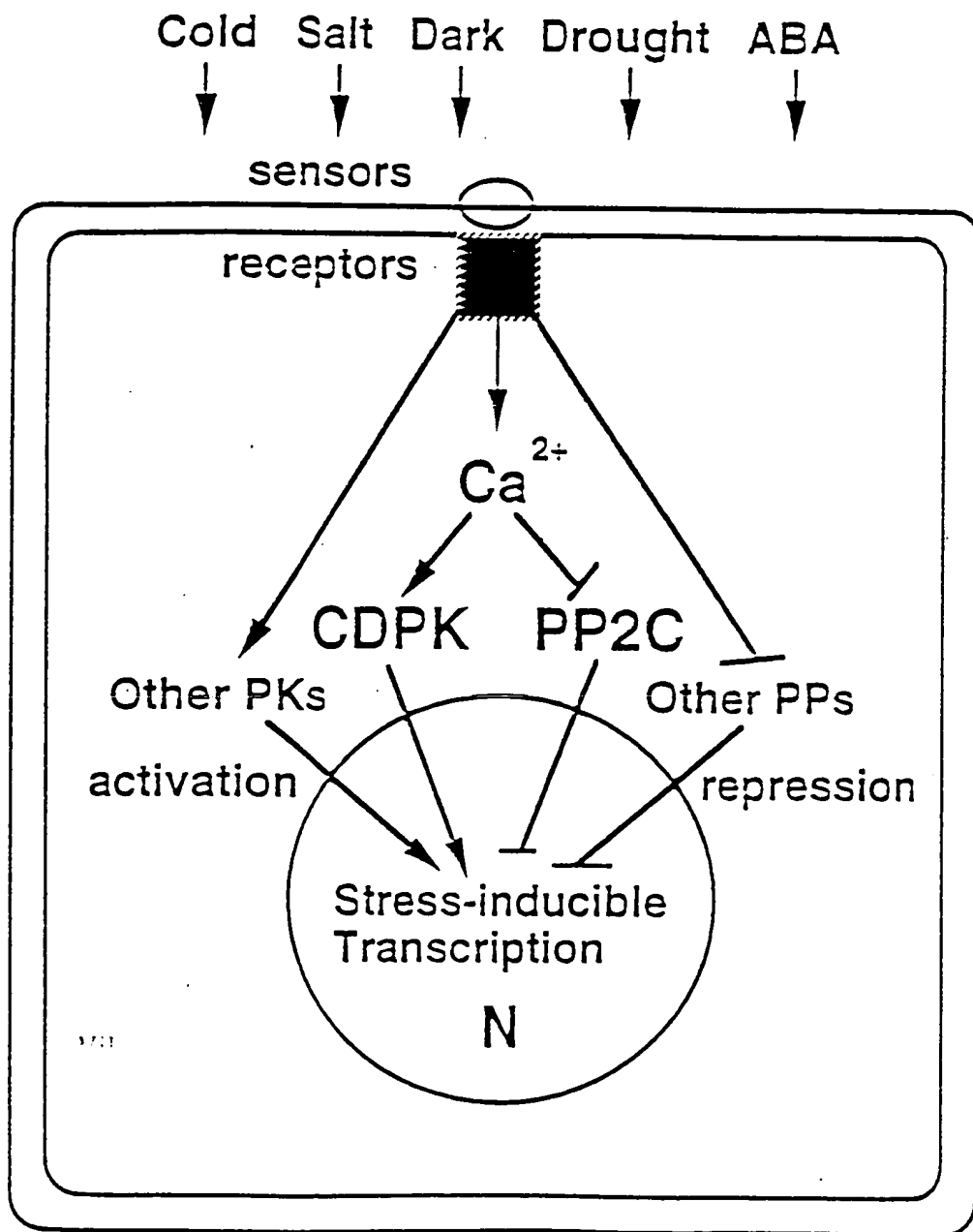


FIG. 4D

FIGURE 5 (SHEET 1/4)

SEQ ID NO: 1 ✓
 1 GTTGTA AAAACGACGGNCAGTGAATTGTAATACGACTCNCCTATAGGGCGNAATTGGAGCTC 60
 -----+-----+-----+-----+-----+
 CAACATTTTGCTGCCNGTCACTTAACATTATGCTGAGNGATATCCCGCCTTAACCTCGAG

a

CACCGCGGTGGCGGCGGCTCTAGAACTAGTGGATCCATGGCTAATCAAACCTCAGATCAGC
 61 -----+-----+-----+-----+-----+ 120
 GTGGCGCCACCGCGGCGGAGATCTTGATCACCTAGGTACCGATTAGTTTGAGTCTAGTCG

SEQ ID NO: 2 → M A N Q T Q I S -

GACAAGTACATCTTAGGACGAGAACTCGGTGCGCGCGGAATTCGGAATCAGGTATCTTTGT
 121 -----+-----+-----+-----+-----+ 180
 CTGTTTCATGTAGAATCCTGCTCTTGAGCCAGCGCGCTTAAGCCTTAGTGCATAGAAACA

a ~ D K Y I L G R E L G R G E F G I T Y L C -

462727-183660

181 ACAGATAGAGAGACTCGTGAAGCTTTAGCTTGCAAATCAATCTCCAAGAGAAAGCTCGGA 240
-----+-----+-----+-----+-----+-----+-----+-----+
TGTCTATCTCTCGAGCACTTCGAAATCGAACGTTTAGTTAGAGGTTCTCTTTCGAGGCT
T D R E T R E A L A C K S I S K R K L R -

241 ACCGCCGTCGATGTGGAAGACGTCGTCGTGAAGTCACGATCATGTCAAACCTTTACCGGAA 300
-----+-----+-----+-----+-----+
TGGCGGCAGCTACACCTTCTGCAGGCAGCACTTCAGTGCTAGTACAGTTGAAATGGCCTT
T A V D V E D V R R E V T I M S T L P E -

301 CACCCAAACGTTGTGAAACTTTAAAGCGACTTATGAGGATAACGAGACCGTGCATCTTTGTG 360
-----+-----+-----+-----+-----+
GTGGGTTTGCAACACATTTGAATTTGGCTGAATACTCCTATTGCTCTGGCACGTAGAACAC
- H P N V V K L K A T Y E D N E T V H L V -

361 ATGGAGCTTTGTGAAGGAGGTGAGCTTTTGGTCGGATTGTTGCAAGAGGACATTATACA 420
-----+-----+-----+-----+-----+
TACCTCGAAACACTTCCTCCACTCGAAAAACCAGCCTAACACGTTCTCCTGTAATATGT
M E L C E G G E L F G R I V A R G H Y T -

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421 GAGCGTGGCGCGGCTACCGTCGCGAGAACGATCGCGGAAGTTGTGAGGATGTGTCAATGTC 480
-----+-----+-----+-----+
CTCGCACGCGCGCGGATGGCAGCGGCTTTGCTAGCGCCTTCAACACTCCTACACAGTACAG
E R A A A T V A R T I A E V V R M C H V -

FIGURE 5 (SHEET 3/4)

AATGGTGTATGCATAGAGATTGGAAGCCTGAGAATTTCTTGTTCCTAACAAGRAGGAG
 481 -----+-----+-----+-----+-----+ 540
 TTACCACAATACGTATCTCTAAACTTCGGACTCTTAAAGAACAACGATTGTTCTTCCTC

a , N G V M H R D L K P E N F L F A N K K E -

AATTCTGCACCTTAAGGCTATTGATTTTGGTTTATCTGTTCCTTTAAACCTGGAGAGAGG
 541 -----+-----+-----+-----+-----+ 600
 TTAAGACGTGAATTCGGATAACTAAAACCAAATAGACAAGAGAAATTTGGACCTCTCTCC

a N S A L K A I D F G L S V L F K P G E R -

TTTACAGAGATTGTTGGAAGTCCTTATTATATGGCTCCAGAAGTGTGGAAGAGAAATTAT
 601 -----+-----+-----+-----+-----+ 660
 AAATGTCTCTAACAACCTTCAGGAATAATATACCGAGGTCTTCACAACCTTCTTTAATA

a F T E I V G S P Y Y M A P E V L K R N Y -

GGACCAGAGGTTGATGTGTGGAGTGCCTGGAGTTATCCTCTACATCTTGCTTTGTGGTGT
 661 -----+-----+-----+-----+-----+ 720
 CCTGGTCTCCAACCTACACACCTCACGACCTCAATAGGAGATGTAGAACGAAACACCAAA

a G P E V D V W S A G V I L Y I L L C G V -

009999-12127

FIGURE 5 (SHEET 4/4)

721 CCTCCGTTTTGGGCAGAGACTGAACAAGGTGTGGCTCTTGGCCATCTGAGGGGAGTTCTT
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 780
 GGAGGCCAAACCCCTCTCTGACTTGTTCACACCGAGAACGGTAGAACTCCCTCAAGAA
 P P F W A E T E Q G V A L A I L R G V L -

781 GATTTTAAGAGAGATCCTTGGTCGCAGATATCAGAGAGCGCAAAGAGCCTTGTGAAGCAG
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 840
 CTAAAATTCTCTCTAGGAACCAGCGTCTATAGTCTCTCGCGTTTCTCGGAACACTTCGTC
 D F K R D P W S Q I S E S A K S L V K Q -

841 ATGTTGGAACCTGATTCAACTAAGCGTTTGACTGCTCAGCAAGTTCTTGATCACCCTTGG
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 900
 TACAACCTTGGACTAAGTTGATTGCGAAACTGACGAGTCGTTCAAGAACTAGTGGGAACC
 M L E P D S T K R L T A Q Q V L D H P W -

901 ATACAGAATGCAAAGAAAGGATCAAGCTTATCGATACCCTCGACCTCGAGGGGGGGCCC
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 960
 TATGTCTTACGTTTCTTTTCCTAGTTGGAATAGCTATGGCAGCTGGAGCTCCCCCCCCGGG
 I Q N A K K

17:1

961 GGTACCAGCTTTNGTTCCCTTTAGTGAGGGTTAATTTGAGCTTGGCGTAATCATGTCAT
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1020
 CCATCGTCAAAANCAAGGGAAATCACTCCCAATTAAAGCTCGAACCGCATTAGTACAGTA

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